Amendments to the Specification:

Please replace the paragraph inserted before the first line of the specification as requested on December 6, 2001 with the following amended paragraph:

This application is a Divisional patent application [~~under 37 C.F.R. § 1.53(b)~~] of [~~Continuation~~] U.S. Application No. 09/506,729, now U.S. Patent 6,365,352, filed on February 18, 2000 [~~(pending allowance)~~], which [~~claims priority to~~] is a continuation of PCT International Application No. PCT/US98/17284, filed August 21, 1998, which claims [~~priority to~~] the benefit of U.S. Provisional Application No. 60/056,844, filed on August 22, 1997, all of which are herein incorporated by reference in their entirety.

Please insert the following paragraph before "**Technical Field**" on page 1, line 5 of the specification:

This application is related to application serial No. 08/510,032, serial No. 60/056,844 and application serial No. 08/688,514, all of which are herein incorporated by reference in their entirety. All published articles, patents and other publications cited throughout this application are herein incorporated by reference in their entirety.

Please replace the paragraph beginning on page 9, line 7, with the following amended paragraph:

Figs. 3A and B Figure 3 is an autoradiogram of the expression profile generated from cDNAs made with RNA isolated from neutrophils exposed to avirulent *E. coli* and virulent and avirulent *Y. pestis*. All possible 12 anchoring oligo d(T)n1, n2 were used to generate a complete expression profile for the enzyme *Bgl*II.

Please replace the paragraph beginning on page 13, line 23, with the following amended paragraph:

The oligonucleotide primer that primes first strand DNA synthesis comprises a 5' sequence incapable of hybridizing to a polyA tail of the mRNAs, and a 3' sequence that hybridizes to a portion of the polyA tail of the mRNAs and at least one non-polyA nucleotide immediately upstream of the polyA tail. The 5' sequence is preferably a sufficient length that can serve as a primer for amplification. The 5' sequence also preferably has an average G+C content and does not contain large palindromic sequence; some palindromes, such as a recognition sequence for a restriction enzyme, may be acceptable. Examples of suitable 5' sequences are

CTCTCAAGGATC[~~÷~~]TACCGCT (SEQ ID [~~No.~~] NO: 1),
CAGGGTAGACGACGCTACGC (SEQ ID [~~No.~~] NO: 2), and
TAATACCGCGCCACATAGCA (SEQ ID [~~No.~~] NO: 3).

Please replace the paragraph beginning on page 15, line 14, with the following amended paragraph:

The adapters for use in the present invention are designed such that the two strands are only partially complementary and only one of the nucleic acid strands that the adapter is ligated to can be amplified. Thus, the adapter is partially double-stranded (*i.e.*, comprising two partially hybridized nucleic acid strands), wherein portions of the two strands are non-complementary to each other and portions of the two strands are complementary to each other. Conceptually, the adapter is "Y-shaped" or "bubble-shaped." When the 5' region is non-paired, the 3' end of other strand cannot be extended by a polymerase to make a complementary copy. The ligated adapter can also be blocked at the 3' end to eliminate extension during subsequent amplifications. Blocking groups include dideoxynucleotides or any other agent capable of blocking the 3'-OH. In this type of adapter ("Y-shaped"), the non-complementary portion of the upper strand of the adapters is preferably a length that can serve as a primer for amplification. As noted above, the non-complementary portion of the lower strand need only be one base, however, a longer sequence is preferable (*e.g.*, 3 to 20 bases; 3 to 15 bases; 5 to 15 bases; or 14 to 24 bases). The complementary portion of the adapter should be long enough to form a duplex under conditions of li[~~ti~~]gation.

Please replace the paragraph beginning on page 23, line 8, with the following amended paragraph:

Synthesis of cDNA was performed as previously described by Prashar *et al.* in WO 97/05286 and in Prashar *et al.* (1996) *Proc. Natl. Acad. Sci. USA* 93:659-663. Briefly, cDNA was synthesized according to the protocol described in the GIBCO/BRL kit for cDNA synthesis. The reaction mixture for first-strand synthesis included 6 μg of total RNA, and 200 ng of a mixture of 1-base anchored oligo(dT) primers with all three possible anchored bases (ACGTAATACGACTCACTATAGGGCGAATTGGGTCGACTTTTTTTTTTTTTTTTTn1 wherein n1=A/C or G, SEQ ID NO: 4) along with other components for first-strand synthesis reaction except reverse transcriptase. This mixture was incubated at 65°C for 5m, chilled on ice and the process repeated. Alternatively, the reaction mixture may include 10μg of total RNA, and 2 pmol of 1 of the 2-base anchored oligo(dT) primers a heel such as RP5.0 (CTCTCAAGGATCTTACCGCTT $_{18}$AT, SEQ ID NO: 5), or RP6.0 (TAATACCGCGCCACATAGCAT $_{18}$CG, SEQ ID NO: 6), or RP9.2 (CAGGGTAGACGACGCTACGCT$_{18}$GA, SEQ ID NO: 7) along with other components for first-strand synthesis reaction except reverse transcriptase. This mixture was then layered with mineral oil and incubated at 65°C for 7 min followed by 50°C for another 7 min. At this stage, 2μl of Superscript reverse transcriptase (200 units/μl; GIBCO/BRL) was added quickly and mixed, and the reaction continued for 1 hr at 45-50°C. Second-strand synthesis was performed at 16°C for 2 hr. At the end of the reaction, the cDNAs were precipitated with ethanol and the yield of cDNA was calculated. In our experiments, ≈200 ng of cDNA was obtained from 10μg of total RNA.

Please replace the paragraph beginning on page 24, line 1, with the following amended paragraph:

The adapter oligonucleotide sequences were A1 (TAGCGTCCGGCGCAGCGACGGCCAG, SEQ ID NO: 8) and A2 (GATCCTGGCCGTCGGCTGTCTGTCGGCGC, SEQ ID NO: 9). One microgram of oligonucleotide A2 was first phosphorylated at the 5′ end using T4 polynucleotide kinase (PNK). After phosphorylation, PNK was heated denatured, and 1μg of the oligonucleotide A1 was

added along with 10× annealing buffer (1 M NaC1/100 mM Tris-HCl, pH8.0/10 mM EDTA, pH8.0) in a final vol of 20 µl. This mixture was then heated at 65°C for 10 min followed by slow cooling to room temperature for 30 min, resulting in formation of the Y adapter at a final concentration of 100 ng/µl. About 20 ng of the cDNA was digested with 4 units of *Bgl* II in a final vol of 10 µl for 30 min at 37°C. Two microliters (≈4 ng of digested cDNA) of this reaction mixture was then used for ligation to 100 ng (≈50-fold) of the Y-shaped adapter in a final vol of 5µl for 16 hr at 15°C. After ligation, the reaction mixture was diluted with water to a final vol of 80 µl (adapter ligated cDNA concentration, ≈50 pg/µl) and heated at 65°C for 10 min to denature T4 DNA ligase, and 2-µl aliquots (with ≈100 pg of cDNA) were used for PCR.

Please replace the paragraph beginning on page 24, line 17, with the following amended paragraph:

The following sets of primers were used for PCR amplification of the adapter ligated 3′ -end cDNAs:

TGAAGCCGAGACGTCGGTCG$(T)_{18}$ n1, n2 (wherein n1, n2 = AA, AC, AG AT CA CC CG CT GA GC GG and GT; SEQ ID NO: 10) as the 3' primer with A1 as the 5' primer or alternatively

RP 5.0, RP 6.0, or RP 9.2 used as 3′ primers with primer A1.1 serving as the 5′ primer. To detect the PCR products on the display gel, 24 pmol of oligonucleotide A1 or A1.1 was 5′ -end-labeled using 15 µl of [γ-^{32} P]ATP (Amersham; 3000 Ci/mmol) and PNK in a final volume of 20 µl for 30 min at 37°C. After heat denaturing PNK at 65°C for 20 min, the labeled oligonucleotide was diluted to a final concentration of 2 µM in 80 µl with unlabeled oligonucleotide A1.1. The PCR mixture (20µl) consisted of 2 µl (≈100 pg) of the template, 2µl of 10× PCR buffer (100 mM Tris·HCl, pH 8.3/500 mM KCl), 2 µl of 15 mM $MgCl_2$ to yield 1.5 mM final Mg^{2+} concentration optimum in the reaction mixture, 200 µM dNTPs, 200 nM each 5′ and 3′ PCR primers, and 1 unit of Amplitaq Gold. Primers and dNTPs were added after preheating the reaction mixture containing the rest of the components at 85°C. This "hot start" PCR was done to avoid ~~artefactual~~ artifactual amplification arising out of arbitrary annealing of PCR primers at lower temperature during transition from room temperature to 94°C in the first PCR cycle. PCR consisted of 5 cycles of 94°C for 30 sec, 55°C for 2 min, and 72°C for 60 sec followed by 25

cycles of 94°C for 30 sec, 60°C for 2 min, and 72°C for 60 sec. A higher number of cycles resulted in smeary gel patterns. PCR products (2.5μl) were analyzed on 6% polyacrylamide sequencing gel. For double or multiple digestion following adapter ligation, 13.2 μl of the ligated cDNA sample was digested with a secondary restriction enzyme(s) in a final vol of 20 μl. From this solution, 3μl was used as template for PCR. This template vol of 3 μl carried ≈ 100 pg of the cDNA and 10 mM $MgCl_2$ (from the 10× enzyme buffer), which diluted to the optimum of 1.5 mM in the final PCR vol of 20 μl. Since Mg^{2+} comes from the restriction enzyme buffer, it was not included in the reaction mixture when amplifying secondarily cut cDNA. Bands were extracted from the display gels as described by Liang *et al.* (1995 *Curr. Opin. Immunol.* 7:274-280), reamplified using the 5′ and 3′ primers, and subcloned into pCR-Script with high efficiency using the PCR-Script cloning kit from Stratagene. Plasmids were sequenced by cycle sequencing on an ABI automated sequencer.

Please replace Table 2, beginning on page 37 with the following Table 2.

TABLE 2

Cln	Sequence
846	1 TCTCAGTGAG CTGAGATCAC ACCACTGCAC TCCAACTGGG CGACAGAGCA 51 AG <u>(SEQ ID NO: 11)</u>
854	1 CACTTTCCCC AAATTCTTTT GCCATAGTTC ACTCTCTACT GATAAGGCCA 51 C. <u>(SEQ ID NO: 12)</u>

855	1 GGGAAAGTGG TGGGGTGGTG AGGGTCAATG TGCAGAAAAT CGATGTAACT 51 TGTAATACAG TTGAGTCAAC TGTGTGTTCA CAACAACTCT GAGAGTTAAC 101 ACCATTTCTA C (SEQ ID NO: 13)
856	1 ATCTAAATAT TTTTCATACC GAGTTATTAA GGAGTCAGTA GTCTGTGCTA 51 CAATGCTGCA AAAAGCATCA CGTGGAAGAA TGGGAACTAT GCGTACTTTA 101 TGAAGTGATG TATAACACAA TGAACTCTGT TTTACAACTA CAGTGCTGCA 151 TTCAATTATC TTCCAT (SEQ ID NO: 14)
859	1 AAGCTCTGTA TACAAAAGTT ATTTATTTAG ATGTTCGAGG CATGTCTCTC 51 CTCACCTGTA AACTAACTGT TTTATAACAG CTTGTATCAC ATGTGTGAAG 101 TTAATGAATG TAATACTCCA ACAAGCCATT CATCAGATTG GCCAACAGCT 151 AGGATACAGT TAAATAATGG CGACCAGGTT GACAAGTCAT AATTGCGGTT 201 TGGGGGACCG TAGTTGCACC TCACCTAGAC CAACGTACGC ATGGCACTCG 251 ACCCAGGCGA ACAAAATTAA T (SEQ ID NO: 15)

863	1 TTTCTCAAGA AGAGATAAGA ATGAAAAGTC ATAGAACACA TCATGGAGGA 51 CCTGGACACA AATGCAGACA AGCAGCTGAG CTTCGAGGAG TTCATCATGC 101 TGATGGCGAG GCTAACCTGG GCCTCCCACG AGAAGATGCA CGAGGGTGAC 151 GATGGCCCTG GCCACCACCA TAAGCCAGGC CTCGGGGAGG GCACCCCCTA 201 AGACCACAGT GGACAAGATC ACAGTGGCCA CGGACACGGC CACAGTCATG 251 GTGGCCACGG CCACAGCCAC TAATCAGGAG GCCAGGCCAC CCTGCCTCTA 301 CCCAACCAGG GCCCCGGGGC CTGTTATGTC AAACTGTCTT GGCTGTGGGG (SEQ ID NO: 16)

866	1 NGATCTTTCT AGGAGGGAGA CACTGGCCNC TCAAATCGTC CAGCGACCTT 51 CCTCATCCAC CCCATCCCTC CCCAGTTCAT TGCACTTTGA TTAGCAGCGG 101 AACAAGGAGT CAGACATTTT AAGATGGTGG CAGTAGAGGC TATGGACAGG 151 GCATGCCACG TGGGCTCATA TGGGGCTGGG AGTAGTTGTC TTTCCTGGCA 201 CTAACGTTGA GCCCCTGGAG GCACTGAAGT GCTTAGTGTA CTTGGAGTAT 251 TGGGGTCTGA CCCCAAACAC CTTCCAGCTC CTGTAACATA CTGGCCTGGA 301 CTGTTTTCTC TCGGCTCCCC ATGTGTCCTG GTTCCCGTTT CTCCACCTAG 351 ACTGTGAACC TCTCGAGGGC AGGGACCACA CCCTGTACTG TTCTGTGTCT 401 TTCACAGCTC CTCCCACAAT GCTGAATATA CAGCAGGTGC TCAATAAATG 451 ATTCT (SEQ ID NO: 17)
871	1 GCAAGTGTGT TGTGTTACAG TGTCACAACA CCGAG (SEQ ID NO: 18)
872	1 GATCTCTCCC TACGCAAAAC GTATTGTAGT GAAAGGGTCT TCTTTACTAC 51 CTTAATAAAA CAGCTAGTGT G (SEQ ID NO: 19)

874	1 GATCTAAATA CAAAGGATAT ACAGTCTTGA ATCTAAAATA ATTTGCTAAC 51 TATTTTGATT CTTCAGAGAG AACTACTA (SEQ ID NO: 20)
876	1 GATCTAGTCC GGACATGCTG TGTATATTGT AACGTTAAAT GAAAAAAGAA 51 CCCCCCTTTG TATTATAGTC ATGCGGTCTT ATGTATGATA AACAGTTG (SEQ ID NO: 21)
878	1 GATCTTTTGT AGTCACCTCT GTATCTTATG TCTGGTTGAG GGGTGCTTTT 51 ACTTGTCTGG CATTTGCATT CAATGATCTT TCAGTCATGT CAGTTAGACT 101 AAAAATTATT TCTG (SEQ ID NO: 22)
880	1 CCCAAGCCCC TTGGACACTG CAGCTCTTTT CAGTTTTTGC TTACACACAA 51 TTCATTCTTT GCAGCTAATT AAGCCGAAGA AGCGTGGGAA TCAAGTTTGG 101 AACAGAGATT AAAAAAGTTC TT (SEQ ID NO: 23)
881	1 GCTCTGGAGG ACAATCCAGG AACTACATTA CCTGGACTGT ATGCTGGTCA 51 TTTCTACAGA CAGCATTCAG TATTTGAGTG TACGGTAACT GTCTGGGGTG 101 ATTCCTATAA GATCATTATA CTG (SEQ ID NO: 24)

882	1 GATCTTTCTC CTTGAATATC TTTCGATAAA CAACAAGGTG GTGTGATCTT 51 AATATATTTG AAAAAAACTT CATTCTCGTG AGTCATTTAA ATGTGTACAA 101 TGTACACACT GGTACTTAGA GTTTCTGTTT GATTCTTTTT TAATAAACTA 151 C (SEQ ID NO: 25)
883	1 TGTCACTCAT GCCCTGGGAC TGCTTCTCCA GCCAGGCGGG CGCCATACGT 51 CCCACACTAG TGAAGGTCAA TGTCTCAGAA CAACACCTCT AT (SEQ ID NO: 26)
884	1 GATCTGGCCT GTTCCTGCGT CTGCGGAGCA GGCCTTGTCT CCCAGCTATC 51 TATAACCTTA CCTAGAGTGT CGACTTGTGG GTTCCTGTTG CTGAGACTTC 101 CTGGATGGAG CCGCCCTCAC CGCCGGACCC GTAGCACTGC GCGGAACTGT 151 GTCCAATAAA GT (SEQ ID NO: 27)
885	1 GATCTGATTT GCTAGTTCTT CCTTGTAGAG TTATAAATGG AAAGATTACA 51 CTATCTGATT AATAGTTTCT TCATACTCTG CATATAATTT GTGGCTGCAG 101 AATATTGTAA TTTGTTGCAC ACTATGTAAC AAAACAACTG AAGATATGTT 151 TAATAAATAT TGTACT (SEQ ID NO: 28)

894	1 GATCTTTATG AGAGCAGTAT TTTCTGTGTT TTCTTTTTAA TTTACAGCCT 51 TTCTTATTTT GATATTTTTT TAATGTTGTG GATGAATGCC AGCTTTCAGA 101 CAGAGCCCAC TTAGCTTGTC CACATGGATC TCAATGCCAA TCCTCCATTC 151 TTCCTCTCCA GATATTTTTG GGAGTGACAA ACATTCTCTC ATCCTACTTA 201 GCCTACCTAG ATTTCTCATG ACGAGTTAAT GCATGTCCGT GGTTGGGTGC 251 ACCTGTAGTT CTGTTTATTG GTCA (SEQ ID NO: 29)
895	1 GATCTAAGTT AGTCCAAAAG CTAAATGATT TAAAGTCAAG TTGTAATGCT 51 AGGCATAAGC ACTCTATAAT ACATTAAATT ATAGGCCGAG CAATTAGGGA 101 ATGTTTCTGA AACATTAAAC TTGTATTTAT GTCACTAAAA TTCTAACACA 151 AACTTAAAAA ATGTGTCTCA TACATATGCT GTACTAGGCT TCATCATGCA 201 TTTCTAAATT TGTGTATGAT TTGAATATAT GAAAGAATTT ATACACGAGT 251 GTTATTTAAA ATTATTAAAA ATAAATGTA (SEQ ID NO: 30)

896	1 GATCTTATAG GCCTGTCTCA TCAGGTTGGT GTCAGCCCAG CTAGGATTAG 51 GCAGAATTGG GTGGGGGCTG TAGTGCACTT TTGGCACAGC ATGTACCTGT 101 CTGACTAATT CTCTGTCTTT TCTTTCCTGT TGCAATTCAT GGGTCTTAGC 151 ATCTTCTGAA TGGTGTTTAG TAGGTCATCC TGTTGATTTC CTGCTAGGGA 201 GTAGCATACT CTGGCTCTGT ACCACTGGCC AAGGGACTTA AGGATAGATG 251 AAGGGCTGCA GTTTTGTTAA ATGGAACAAT ATGAAGAGA (SEQ ID NO: 31)
T103	1 GATCTTTCTC CTTGAGTATC TTTCGATAAA CAACAAAGTG GTGTGATCTT 51 AATATATTTG AAAAAAACTT CATTCTCGTG AGTCATTTAA ATGTGTACAA 101 TGTACACACT GGTACTTAGA GTTTCTGTTT GATTCTTTTT TAATAAACTA 151 C (SEQ ID NO: 32)
T104	1 GATCTCTGCT CATAGAATGC ATGGGGAGCC TTCCAGCTCA CTCTCCCTGA 51 GGACTGGCTT GACAGGGGCT ATGGGTTTGC TTTGG (SEQ ID NO: 33)

T10 5	1 GATCTGCGCT TCCAGAGCGC AGCTATCGGT GCTTTGCAGG AGGCAAGTGA 51 GGCCTATCTG GTTGGCCTTT TTGAAGACAC CAACCTGTGT GCTATCCATG 101 CCAAACGTGT AACAATTATG CCAAAAGACA TCCAGCTAGC ACGCCGCATA 151 CGTGGAGAAC GTGCTTAAGA ATCCACTATG ATGGGAAACA (SEQ ID NO: 34)
T10 7	1 GATCTAAATG TGAACAGTTT ACTAATGCAC TACTGAAGTT TAAATCTGTG 51 GCACAATCAA TGTAAGCATG GGGTTTGTTT CTCTAAATTG ATTTGTAATC 101 TGAAATTACT GAACAACTCC TATTCCCATT TTTGCTAAAC TCAATTTCTG 151 GTTTTGGTAT ATATCCATTC CAGCTTAATG CCTCTAATTT TAATGCCAAC 201 AAAATTGGTT GTAATCAAAT TTTAAAATAA TAATAATTTG GC (SEQ ID NO: 35)
T76	1 GCCTTTTCGA TAGTTTCGGG TCAGGTAAAA ATGGCCTCCT GGCGTAAGCT 51 TTTCAAGGTT TTTTGGAGGC TTTTTGTAAA TTGTGATAGG AACTTTGGAC 101 CTTGAACTTA CGTATCATGT GGAGAAGAGC CAATTTAACA AACTAGGAAG 151 ATGAAAAGGG AAATTGTGGC CAAAACTTTG GGAAAAGGAG GTTCTTAAAA 201 TCAGTGTTTC CCCTTT (SEQ ID NO: 36)

T8	1 GATCTATGCA CAAGAACCCC TTTACCCCAT GACCAACATC GCAGACACAT 51 GTGCTGGCCA CCTGCTGAGC CCCAAGTGGA ACGAGACAAG CAGCCCTTAG 101 CCCTTCCCCT CTGCAGCTTC CAGGCTGGCG TGCAGCATCA GCATCCCTAG 151 AAAGCCATGT GCAGCCACCA GTCCATTGGG CAGGCAGATG TTCCTAATAA 201 AGCT <u>(SEQ ID NO: 37)</u>
T81	1 GATCTTTCCT CCTGGTTACT GTGAAGCCTG TTGGTTTGCT GCTGTCGTTT 51 TTGAGGAGGG CCCATGGGGG TAGGAGCAGT TGAACCTGGG AACAAACCTC 101 ACTTGAGCTG TGCCTAGACA ATGTGAATTC CTGTGTTGCT AACAGAAGTG 151 GCCTGTAAGC TCCTGTGCTC CGGAGGGAAG CATTTCCTGG TAGGCTTTGA 201 TTTTTCTGTG TGTTAAAGAA ATTCAATCTA CTCATGATGT GTTATGCATA 251 AAACATTTCT GGAACATGGA TTTGTGTTCA CCTTAAATGT GAAAATAAAT 301 CCTA <u>(SEQ ID NO: 38)</u>

T82	1 ATCTTTCCTC CTGGTTACTG TGAAGCCTGT TGGTTTGCTG CTGTCGTTTT 51 TGAGGAGGGC CCATGGGGGT AGGAGCAGTT GAACCTGGGA ACAAACCTCA 101 CTTGAGCTGT GCCTAGACAA TGTGAATTCC TGTGTTGCTA ACAGAAGTGG 151 CCTGTAAGCT CCTGTGCTCC GGAGGGAAGC ATTTCCTGGT AGGCTTTGAT 201 TTTTCTGTGT GTTAAAGAAA TTCAATCTAC TCATGATGTG TTATGCATAA 251 AACATTTCTG GAACATGGAT TTGTGTTCAC CTTAAATGTG AAAATAAATC 301 CTATTTTCTA TG (SEQ ID NO: 39)

T85	1 GATCTTTGGC AGCGCCATTG GACTCTTTGG GGTCATCGTC GCAATTCTTC 51 ATACCTCCAG AGTGAAGATG GGTGACTAGA TGATATGTGT GGGTGGGGCC 101 GTGCCTCACT TTTATTTATT GCTGGTTTTC CTGGGACAGC TGGAGCTGTG 151 TCCCTTAACC TTTCAGAGGC TTGGTGTTCA GGGCCCTCCC TGCACTCCCC 201 TCTTGCTGCG TGTTGATTTG GAGGCACTGC AGTCCAGGCC GAGTCCTCAG 251 TGCGGGGAGC AGGCTGCTGC TGCTGACTCT GTGCAGCTGC GCACCTGTGT 301 CCCCCACCTC CACCCTCAAC CCATCTTCCT AGTGTTTGTG AAATAAACTT 351 GGTAT (SEQ ID NO: 40)
T98	1 GATCTTCCAC GTCTCCATCT CAGTACACAA TCATTTAATA TTTCCCTGTC 51 TTACCCCTAT TCAAGCAACT AGAGGCCAGA AAATGGGCAA ATTATCACTA 101 ACAGGTCTTT GACTCAGGTT CCAGTAGTTC ATTCTAATGC CTAGATTCTT 151 TTGTGGTTGT TGCTGGCCCA ATGAGTCCCT AGTCACATCC CCTGCCAGAG 201 GGAGTTCTTC TTTTGTGAGA GACACTGTAA ACGACACAAG AGAACAAGAA 251 TAAAA (SEQ ID NO: 41)

933	1 TTATATATTT TTCTTAAATA TGTTTTATTG TCTTCTCTAA GCAAAAAGTT 51 CTTAATAAAC ATAGTATTTC TCTCTGCGTC CTATTTCATT AGTGAAGACA 101 TAGTTCACCT AAAATGGCAT CCTGCTCTGA ATCTAGACTT TTTAGAAATG 151 GCATATGTTT TTGATGATAT GTCAACATTC AAAATAGTCC TAATTAAATT 201 GTTGGTTAAA TGTAATGTCA ACTCTTTATA AACTTAAATA TAAACAAGTA 251 ATTAACCACT CTAAGTAATA AAACACATTT CACCTGTGTT CTGAGTGTA (SEQ ID NO: 42)

967	1 ATGAATCCTT GCCACCTCCA CCTGCAGAAC TGTTATAAAT ATTACAACTT 51 GCTTTTTAGC TGATCTTCCA TCCTCAAATG ACTCTTTTTT CTTTATATGT 101 TAACATATAT AAAATGGCAA CTGATAGTCA ATTTTGATTT TTATTCAGGA 151 ACTATCTGAA ATCTGCTCAG AGCCTATGTG CATAGATGAA ACTTTTTTTT 201 AAAAAAAGTT ATTTAACAGT AATCTATTTA CTAATTATAG TACCTATCTT 251 TAAAGTATAG TACATTTTAC ATATGTAAAT GGTATGTTTC AATAATTTAA 301 GAACTCTGAA ACAATCTACA TATACTTATT ACCCAGTACA GTTTTTTTTC 351 CCCTGAAAAG CTGTGTATAA AATTATGGTG AATAAACTTT TATGTTTCCA 401 TTTCAAAGAC CAGGGTGGAG AGGAATAAGA GACTAAGTAT ATGCTTCAAG 451 TTTTAAATTA ATACCTCAGG TATTAAAATA AATATTCCAA GTTTGTGGGA 501 AATGGGGAGA TTAAAATG (SEQ ID NO: 43)

978	1 TTATGTGGCC TTAGGTAGCT GGTTGTACAT CTTTCCCTAA ATCGATCCAT 51 GTTACCACAT AGTAGTTTTA GTTTAGGATT CAGTAACAGT GAAGTGTTTA 101 CTATGTGCAA CGGTATTGAA GTTCTTATGA CCACAGATCA TCAGTACTGT 151 TGTCTCATGT AATGCTAAAA CTGAAATGGT CCGTGTTTGC ATTGTTAAAA 201 ATGATGTGTG AAATAGAATG AGTGCTATGG TGTTGAAAAC TGCAGTGTCC 251 GTTATGAGTG CCAAAAATCT GTCTTGAAGG CAGCTACACT TTGAAGTGGT 301 CTTTGAATAC TTTTAATAAA TTTATTTTGA TA (SEQ ID NO: 44)

981	1 TAGGTGAACC CTTATTCTGC AGGGTTCTCC CTCCCACCTT AAAGAAGTTC 51 CCCTTATGTG GGTTGCCTGG TGAATGGCCT TCCTTCCCGC CAGAGGGCTT 101 GTGAACAGAC CGGAGAGGAC AGTGGATTGT TTATACTCCA GTGTACATAG 151 TGTAATGTAG CGTGTTTACA TGTGTAGCCT ATGTTGTGGT CCATCAGCCC 201 CTCACATTCC TAGGGGTTTG AGATGCTGTA CGTGGTATGT GACACCAAAG 251 CCACCTCTGT CATTTGTTGT GATGTCTTTT CTTGGCAAAA GCCTTGTGTA 301 TATTTGTATA TTACACATTT GTACAGAATT TTGGAAGATT TTCAGTCTAG 351 TTGCCAAATC TGGCTCCTTT ACAAAAG (SEQ ID NO: 45)

982	1 AGAATCTCTT ATGTTCTCAG AGGAAGGTGG AAGAAACCAT GGGCAGGAGT 51 AGGAATTGAG TGATAAACAA TTGGGCTAAT GAAGAAAACT TCTCTTATTG 101 TTCAGTTCAT CCAGATTATA ACTTCAATGG GACACTTTAG ACCATTAGAC 151 AATTGACACT GGATTAAACA AATTCACATA ATGCCAAATA CACAATGTAT 201 TTATAGCAAC GTATAATTTG CAAAGATGGA CTTTAAAAGA TGCTGTGTAA 251 CTAAACTGAA ATAATTCAAT TACTTATTAT TTAGAATGTT AAAGCTTATG 301 ATAGTCTTTT CTAATTCTTA ACACTCATAC TTGAAATCTT TCTGAGTTTC 351 CCCAGAAGAG AATATGGGAT TTTTTTTGAC ATTTTTGACT CATTTAATAA 401 TGCTCTTGTG TTTACCTAGT ATATGTAGAC TTTGTCTTAT GTGTCAAAAG 451 TCCTAGGAAA GTGGTTGATG TTTCTTATAG CAATTAAAAA TTATT (SEQ ID NO: 46)

905	1 ATCTCAGTGA GCTGAGATCA CACCACTGCA CTCCAACTGG GCGACAGAGC 51 AAGA (SEQ ID NO: 47)

910	1 GATCTGTAAT TCAGGTGTTT TCTGTACAGC CATACGTAGA TAATGAAGCC 51 AAAAGGCTTT TAATTACACC ATGGCCTAAA ATAAATTCAT CA (SEQ ID NO: 48)
915	1 TATTTTTCAG CTGAGTTATT AGGGAGTCAT TATTCTGTGG TACAATGCTG 51 CAAAAAGCAT CATGTGGAAG AATGGGAACT ATGCTTACAT TATGAAGTGA 101 TGTATAACAC AATGCAAATC TG (SEQ ID NO: 49)
916	1 GATCTTTTTT CATTAAAAAA TGTTCAATTA TCAGGCCGGG TGCAGTGGGG 51 CTCATGCCTG TAATCCCAAC ACTTTGGGAG GCCGATGCAG GCGGATCACT 101 AGGTCAGCAG ATCGAGACCA TCCTGGCTAA CACAGTGAAA CCT (SEQ ID NO: 50)
921	1 GATCTTTATT TTTAGCCATG CACTGTTGTG AGGAAAATTA CCTGTCTTGA 51 CTGCCATGTG TTCATCATCT TAAGTATTGT AAGCTGCTAT GTATGGATTT 101 AAACCGTAAT CATATCTTTT TCCTATCTAT CTGAGGCACT GGTGGAATAA 151 AGAACCTGTA TATTTTACTT TGTTGCAGAT AGTCTTGCCG CATCTTGGCA 201 AGTTGCAGAG A (SEQ ID NO: 51)

927	1 GATCTTCGTG AAGACCTGAC TGGTAAGACC ATCACCCTCG AGGTGGAGCC 51 CAGTGACACC ATCGAGAATG TCAAGGCAAA GATCCAAGAT AAGGAAGGCA 101 TCCCTCCTGA TCAGCAGAGG TTGATCTTTG CTGGGAAACA GCTGGAAGAT 151 GGACGCACCC TGTCTGACTA CAACATCCAG AAAGAGTCCA CTCTGCACTT 201 GGTCCTGCGC TTGAGGGGGG GTGTCTAAGT TTCCCCTTTT AAGGTTTCAA 251 CAAATTTCAT TGCACTTTCC TTTCAATAAA GTTG (SEQ ID NO: 52)
928	1 GATCTTTCCT CCTGGTTACT GTGAAGCCTG TTGGTTTGCT GCTGTCGTTT 51 TTGAGGAGGG CCCATGGGGG TAGGAGCAGT TGAACCTGGG AACAAACCTC 101 ACTTGAGCTG TGCCTAGACA ATGTGAATTC CTGTGTTGCT AACAGAAGTG 151 GCCTGTAAGC TCCTGTGCTC CGGAGGGAAG CATTTCCTGG TAGGCTTTGA 201 TTTTTCTGTG TGTTAAAGAA ATTCAATCTA CTCATGATGT GTTATGCATA 251 AAACATTTCT GGAACATGGA TTTGTGTTCA CCTTAAATGT GAAAATAAAT (SEQ ID NO: 53)

930	1 GATCTTTCGG GTTCTCTCTC CTAACTCAGC TCTTCGTTCC CAGAAACCCA 51 GATGTAATCC CCCTACGTGG TGCTTGGGGC ATCCCGATAC CATCTCAGTA 101 AATCTCCTAC ATTGGCCTCC TCACCCTCCC CGGGACCCAC ACCCTTCAGG 151 TCCTCACCCT GAGACAGGAG GGACCCTCTG AGATCAGGGA CCCTTAGGTC 201 TCACTGCTCT CTGATTCATA GCTCAACTGG GCCCCCAGTT CCATACCCCA 251 GCATTCCCGG TCACTCCCTC CCTAATCTGA GCATCACTCA AGCTCTTTAT 301 TAAACTC (SEQ ID NO: 54)
939	1 ATCTCTCTCC CTACGCAAAA CCCTATTGTA GTAAAAAAGT CTTCTTTACT 51 ATCTTAATAA AACAGATATT GTG (SEQ ID NO: 55)
945	1 ATCTATTCTT GTAGATTTTT TTTGTGTGGG TCTATGTTTC ATTCATCTGC 51 TTTCAGGCTG GATTTATAAC AAGCAGAACT TTTAAAACG (SEQ ID NO: 56)
949	1 GATCTAAATA TTTTTCAGCT GAGTTATTAC GGAGTCATTA TTCTGTGGTA 51 CAATGCTGCA AAAAGCATCA TGTGGAAGAA TGGGAACTAT GCTTACTTTA 101 TGAAGTGATG TATAACACAA TGAAA (SEQ ID NO: 57)

952	1 CTACCCCGTG ACTCAGTTAC CTCCCACTGG GTCCCTCCCA CATCATGTGG 51 GAATTGTAGG AGCTACAATT CAAGATGAGA TTTGGATGGG GTCACAGCCA 101 AACCATATCA CTGAGGTATC AAGGAGATTC TT (SEQ ID NO: 58)
954	1 GATCTGATTT GCTAGTTCTT CCTTGTAGAG TTATAAATGG AAAGATTACA 51 CTATCTGATT AATAGTTTCT TCATACTCTG CATATAATTT GTGGCTGCAG 101 AATATTGTAA TTTGTTGCAC ACTATGTAAC AAAACAACTG AAGATATGTT 151 TAATAAATAT TGTACTTATT G (SEQ ID NO: 59)
975	1 NGATCTTTCT CCTTGAATAT CTTTCGATAA ACAACAAGGT GGTGTGATCT 51 TAATATATTT GAAAAAAACT TCATTCTCGT GAGTCATTTA AATGTGTACA 101 ATGTACACAC TGGTACTTAG AGTTTCTGTT TGATTCTTTT TTAATAAA (SEQ ID NO: 60)

976	1 GATCTGCTAG AAGATGGTTT TGGAGAGCAC CCCTTTTACC ACTGCCTGGT 51 TGCAGAAGTG CCGAAAGAGC ACTGGACTCC GGAAGGTAAC CCCTCGCCCT 101 TTCCAGAAGC CAGAGAGACC AAGTGTTATG TAAGAAGTAG TGTCGGCTGT 151 GTAGAACCAC TGACTACACA GGCCGAAGTT ACTGAGAACT TGGACAGAAA 201 AAATAGCCAG CAAGTGTT (SEQ ID NO: 61)
984	1 CATTCACACA TTTAACCTCC TTCCATACCA AATCTT (SEQ ID NO: 62)
986	1 GATCTGGACA GCAGAATGTT ATAACGCAAG TTCATGTGTT GCTCCCAACT 51 CCATTCTCTT TTCTCTCGTG CAACCAGTTT GCCCATTCTC TTCCTATTAC 101 TTGCTC (SEQ ID NO: 63)
T11 3	1 TCAGAGATTT GCAAAGACTC ACGTTTTTGT TGTTTTCTCA TCATTCCATT 51 GTGATACTAA GAAACTAAGA AGCTTAATGA AAAGAAATAA AATGCCTATG (SEQ ID NO: 64)

T116	1 GATCTGCGCT TCCAGAGCGC AGCTATCGGT GCTTTGCAGG AGGCAAGTGA 51 GGCCTATCTG GTTGGCCTTT TTGAAGACAC CAACCTGTGT GCTATCCATG 101 CCAAACGTGT AACAATTATG CCAAAAGACA TCCAGCTAGC ACGCCGCATA 151 CGTGGAGAAC GTGCTTAAGA ATCCACTATG ATGGGAAACA (SEQ ID NO: 65)
T123	1 GATCTGTGAA ATGCTATCTC TCCTGAAGCA ATACTGTTGA CCAGAAAGGA 51 CACTCCATAT TGTGAAACCG GCCTAATTTT TCTGACTGAT ATGGAAACGA 101 TTGCCAACAC ATACTTCTAC TTTTAAATAA ACAACTTTGA TGATGTAACT 151 TGACCTTCCA GAGTTATGGA AATTTTGTCC CCATGTAATG AATAAATTGT 201 ATGTAT (SEQ ID NO: 66)